Count Data Regression: Negative Binomial GLMs

STAT 245

Negative Binomial Distributions

- Can be used to model count data
- Have two parameters:
 - \circ a mean μ (like the Poisson "rate" λ)
 - \circ dispersion parameter α (relates μ and variance)
- NB1: variance is linear function of μ
- NB2: variance is quadratic function of μ
- Won't detail equation, likelihood as much

Profiles in Stats: Mollie Brooks



- Developer of glmmTMB package
- Techn. Uni. Denmark
- Ecosystem-based marine management

NB Regression in R

```
library(glmmTMB)
theft nb1 <- glmmTMB(Thefts ~ NEnrollment + Location
                 TrainingHours + SecurityCameras,
               data = sscrime,
               family = nbinom1(link = 'log'))
theft nb2 <- glmmTMB(Thefts ~ NEnrollment + Location
                 TrainingHours + SecurityCameras, 4 / 17
```

How far off from Poisson mean = var?

```
summary(theft_nb1)
```

```
Family: nbinom1 ( log )
## Formula:
## Thefts ~ NEnrollment + Location + TrainingHours + SecurityCameras
## Data: sscrime
##
##
       AIC
               BIC logLik deviance df.resid
    2587.9 2619.5 -1286.0
                           2571.9
##
                                        373
##
##
## Dispersion parameter for nbinom1 family (): 8.88
##
## Conditional model:
                       Estimate Std. Error z value Pr(>|z|)
##
## (Intercept)
                               1.239e-01 17.322 < 2e-16 ***
                      2.146e+00
## NEnrollment
                      1.998e-04 2.799e-05 7.140 9.32e-13 ***
                     -1.509e-01 1.418e-01 -1.065
## LocationTown
                                                   0.2870
## LocationUrban Fringe -3.484e-02 1.026e-01 -0.340 0.7342
## LocationDural
```

NB1 vs. NB2

Suggestion: use scaled residual plot or maybe IC to choose, if no domain knowledge suggesting one

Which fits better?

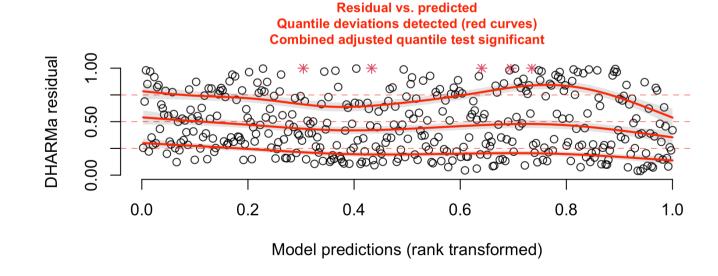
Much better than Poiss.

Don't use IC to compare Pois/NB; just USE NB1 or 2, almost always.

Assessment w/DHARMa scaled residuals?

Uniform vertically -> mean-var relationship well modelled

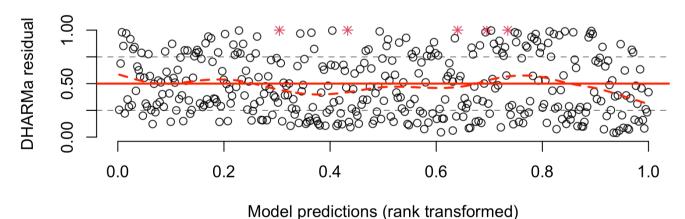
```
library(DHARMa)
nb2_sim <- simulateResiduals(theft_nb2)
plotResiduals(nb2_sim)</pre>
```



Assessment w/DHARMa scaled residuals?

Uniform vertically -> mean-var relationship well modelled

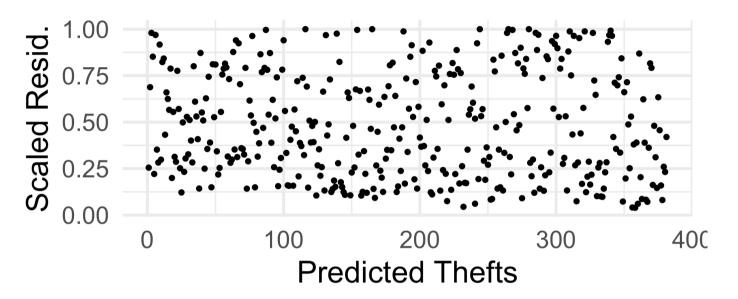
Residual vs. predicted



Assessment w/DHARMa scaled residuals Uniform vertically -> mean-var relationship well modelled

Assessment w/scaled residuals?

Uniform vertically -> mean-var relationship well modelled



More Assessment needs doing!

- Check ACF for independence of residuals
- No need to check residual histogram
- Check log(response) vs. predictors and scaled residuals vs fitted and vs predictors for trends (linearity)

Next: Offsets; Model selection; interactions

Offsets

What if we need to model counts per something?

- Thefts per school per student (instead of using NEnrollment as predictor, essentially model Thefts / NEnrollment)
- Animal sightings *per unit effort* (sites checked; miles on trackline)

Offsets: Math

$$log(\frac{\lambda_i}{ ext{effort}}) = \beta_0 + \dots$$

is the same as...

$$log(\lambda_i) = \beta_0 + \cdots + log(effort)$$

Offsets in R

(Use your smarts to decide if one is needed: NOT IC. Why?)

```
theft_nb2_offs <- glmmTMB(Thefts ~ Location +
                 TrainingHours + SecurityCameras +
                 offset(log(NEnrollment)),
                 data = sscrime,
                 family = nbinom2(link='log'),
                 na.action = 'na.fail')
```

Technical note: if using dredge() to make IC comparisons, tell dredge() to always include the offset term!

```
theft nb2 offs <- update(theft nb2 offs,
                         na.action = 'na.fail')
library(MuMIn)
dredge(theft nb2 offs,
       rank = 'BIC',
       fixed = 'cond(offset(log(NEnrollment)))')
```

omit the cond() if using a Poisson GLM fitted via glm()